1. (Amended) A method for comparing a test genome to a reference genome, said method comprising:

(i) providing a plurality of clones of known size that substantially cover at least a portion of said test genome;

(ii) obtaining sequence information from the termini of each of said plurality of clones, thereby obtaining a pair of terminal sequences;

(iii) identifying a pair of sequences within said reference genome that corresponds to each of said pairs of terminal sequences; and

(iv) determining the relationship between the members of each pair of corresponding sequences within said reference genome;

wherein a difference in the observed relationship between the members of any of said pairs of corresponding sequences within said reference genome and the expected relationship based upon said known size of said plurality of clones indicates the presence of a rearrangement in said test genome compared to said reference genome and wherein said test genome is obtained from an individual with a disease.

REMARKS

Status:

Claims 1-6 and 10-23 are pending and under consideration after entry of this Amendment, no claims being added, claim 1 being amended and claims 7-9 being canceled herein. Support for the amendment to claim 1 may be found in the specification at least on page 6, lines 18-20. No new matter is added by this amendment.

Claims 7-9 were objected to under 37 C.F.R. §1.75 (c) as allegedly improper dependent claims. Claims 1-23 were rejected under 35 U.S.C. §112, second paragraph as allegedly indefinite. Claims 1, 3, and 11 were rejected under 35 U.S.C. §102(b) on the basis that they are anticipated by Brosch *et al., Infection and Immunity* 66: 2221-2229 (1998) ("Brosch") or Mahairas *et al., Proc. Nat. Acad. Sci. USA* 96: 9739-9744 (1999) ("Mahairas"). Claim 1 is rejected under 35 U.S.C. §103(a) as allegedly